

1990

1	GTGACTCATGCTGTTGAACTTACTGTCAACAGCACTGTAACCTCATGCCTGAGCCAAGC	60
61	TTGTCTAACACGTATATTTTCTCTGTAAAGCACATCACAGCCTTTCTGCACTTAGGAACA	120
121	TTAGACAGCACTTCAGCAGTACACTTGGGGGCCATTTTAAACAATTAAATCACTGATAGG	180
181	CTCCGCTCCGCTCAGGGCGGGCCCCAGACACGGGTTTCCCATGGCAGCACCACGGCAGGCC	240
241	CGGCGCACCTGCTGCCCCGAACCCCTGGCTCCAGGGGGCAATGAGGGGGCAGTGGAAGGG	300
301	GCACTACTCCTCGGGCATTGCCTAGAGAAGCGAGACCGTCCCGCCCTCCCGCTGGCCCTC	360
361	CTTCTCTCCCGCCCGGGGCGCGCAATTCTCCGCCAGAGGGACAGTCGGCCTCATATGT	420
1		M L 2
421	TAAGACCTCTGATCACTAGATCCCCTGCATCTCCACTGAACAACCAAGGCACCCCTACTC	480
3	R P L I T R S P A S P L N N Q G T P T P	22
481	CGGCACAACCTCACAAAATCCAATGCGCATGTCCACACTGATGTGGGCAGCCACATGTACA	540
23	A Q L T K S N <u>A H V H T D V G S H M Y T</u>	42
541	CCAGCAGCCTGGCCACCCTCACAAATACCCTGTATCCAGAATCAGAAGACTTTGTGATG	600
43	<u>S S L A T L T K Y P V S R I R R L C D G</u>	62
601	GTACAGAGCCCATAGTTTTGGACAGTCTCAAACAGCACTATTTCACTGACAGAGATGGAC	660
63	<u>T E P I V L D S L K Q H Y F T D R D G Q</u>	82
661	AGATGTTTCAATATATCTTGAATTTTCTACGAACATCCAAACTCCTCATTCTTGATGATT	720
83	<u>M F R Y I L N F L R T S K L L I L D D F</u>	102
721	TCAAGGACTACACTTTGTTATATGAAGAGGCAAAATATTTTCAGCTTCAGCCCATGTTGT	780
103	<u>K D Y T L L Y E E A K Y F Q L Q P M L L</u>	122
781	TGGAGATGGAAGATGGAAGCAGGACAGAGAACTGGTCGCTTTTCAAGGCCCTGTGAGT	840
123	<u>E M E R W K Q D R E</u> T G R F S R P C E C	142
841	GCCTTGTTTGTGTGGCCCCAGACCTCAGAGAAAGGATCACGCTAAGTGGTGACAAATCCT	900
143	L V C V A P D L R E R I T L S G D K S L	162
901	TGGTAGAAGAAGTGTTTCCAGAGATCGGCGATGTGATGTGCAACTTTATCAGTGCAGGCT	960
163	V E E V F P E I G D V M C N F I S A G W	182

Figure 1B

961	GGAATCATGACTCCACGCACATCGTCAGGTTTCCACTAAGTGGCTACTGTCACCTCAACT	1020
183	N H D S T H I V R F P L S G Y C H L N S	202
1021	CAGTCCAGGTCCTCGAGAGGTTGCAGCAAAGAGGATTTGAAATCGTGGGCTCCTGTAGGG	1080
203	V Q V L E R L Q Q R G F E I V G S C R G	222
1081	GAGGAGTGGGCTCATCCTAGTTCAGCAAATACGTCCTTCATAGGGAAGTGGGCGGATGC	1140
223	G V G S S	227
1141	CCTCCCGTACCCTCCATCATCTGGATAAAGCAAGAGCCTCTGGACTAAACGGACATATTT	1200
1201	CTTATGCAAAAAGGAAAACACACACAACTAATAAACAAATAATAAAAAAGGGACATTTGT	1260
1261	GTGCAGTTGGGACAGAAAACCAAGTCCTGCACCTAAAATTGAATAAAAGATGCATTTATA	1320
1321	TGCAATAGAGACCACACCTGTATTCATATGGAACAATTGAATAGTTCACTCAAAAAA	1380
1381	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1418

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Figure 2

		1		50
K+betaM3	(1)	-----		
MECHP-2	(1)	-----		
KCNMB1	(1)	-----		
CG10465	(1)	-----		
CG10440	(1)	MDRERERDVKALEPRDLSSSTGRIYARSDIKISSSPTVSPTISNSSSPTPT		
		51		100
K+betaM3	(1)	-----MLRPLITRSPASPIINNQ-----		GTPTPAQ
MECHP-2	(1)	-----MSRPLITRSPASPIINNQ-----		GIPTPAQ
KCNMB1	(1)	-----		
CG10465	(1)	-----MSESMSGD-----		HKILL
CG10440	(51)	PPASSSVTPPLGLPGAVAAAAAVGGASSAGASSYLHGNHKPITGIPCVA		
		101		150
K+betaM3	(25)	LTKSNAHVHTDVGSHMYTSSLATLTQYVVSRTIRLCDGTEPIVLDSLQKH		
MECHP-2	(25)	LTKSNAHVHTDVGSHMYTSSLATLTQYVESRIGRLFDGTEPIVLDSLQKH		
KCNMB1	(1)	-----VVKQLVMAQKRCEITRALCLGVTMVCAVITYYTLVITVLPPLYQ		
CG10465	(14)	KCHSSQYLKCNVGGHLYYITIGTLTKNNDIMISAMESGRMEVITDS-EGW		
CG10440	(101)	ASRYTAPVHTDVGGLTYTSSLETLTQYVESKRLKLFNGQPIVLDSLQKH		
		151		200
K+betaM3	(75)	YFIDRDGOMFRMYILNFLRTSKLLILDFDKDYTLLEYEAKYEQLOPMLLEM		
MECHP-2	(75)	YFIDRDGOMFRMYILNFLRTSKLLIPDFDKDYTLLEYEAKYEQLOPMLLEM		
KCNMB1	(44)	KSVWTOESKCHLIETNIRDOEELGKKVPOYPCLWNVNSAAGRWAYLYHT		
CG10465	(63)	ILIDRCCNHFGIILNMLRDGTVPFPETNKEIAELLAEAKYCTITELALSC		
CG10440	(151)	YFIDRDGOMFRMYILNFMNRNRLILIAEDFPDLLELEYEARYEVEPMTKQIL		
		201		250
K+betaM3	(125)	ERWKQDRETG-----RFSRPECIVC-----		
MECHP-2	(125)	ERWKQDRETG-----RFSRPECIVVR-----		
KCNMB1	(94)	EDTRDQNNQC-----S-----		
CG10465	(113)	ERALYAHQEPKPICRIPLITSQ--KEEQLLLSVSLKPAVILVQRQNNKY		
CG10440	(201)	ESMRKDRVRNGNYLVAPPTPPARHIKTSPTSASPECNYEVVALH----		
		251		300
K+betaM3	(146)	-----VAPDLRERITLSCDKS-----LVEEVFP		
MECHP-2	(147)	-----VAPDLGERITLSCDKS-----LVEEVFP		
KCNMB1	(105)	-----YIPGSVDNYQTARADVKK-----VRAKFQ		
CG10465	(161)	SYTSTSDNLLKNIELFDKLSLRINERILFIKDVIGPSEICCWSEYGHGK		
CG10440	(246)	-----ISPDLGERIMLSARA-----LDELFP		
		301		350
K+betaM3	(169)	EIGDVMCNFTIS-AGWNH-----DSTHIVRFPLSGYCHLNSVQVLERLQQ		
MECHP-2	(170)	EIGDVMCNFVN-AGWNH-----DSTHIVRFPLSGYCHLNSVQVLERLQQ		
KCNMB1	(129)	EQQVFYCFSAAP--R-GNE-----TSVLFRQRYGPAALLFSIFWPTFLIT		
CG10465	(211)	KVAELVCCTSIIVYATDRKHTKVEFPETARYEETLQVLLYENRNAPDOELMQ		
CG10440	(269)	EASQATQSSRSGVSWNQG----DWGQITRFPLNGYCKLNSVQVLTRLLN		
		351		395
K+betaM3	(212)	RGFEIVGSCRGGVGSS-----		
MECHP-2	(213)	RGFEIVGSCCGGVDS--OFSEYVLRRELRRTPRVPSVIRIKQEPLD		
KCNMB1	(170)	CGLLILAMVKS-----NOYLSITLAAQ		
CG10465	(261)	ATSSARVGSASGTSINNOYISDEEEERTGLARLRSNKRNNPS----		
CG10440	(314)	AGFTIEASVCG-----OOFSEYTLARRVPM-----		

Figure 3

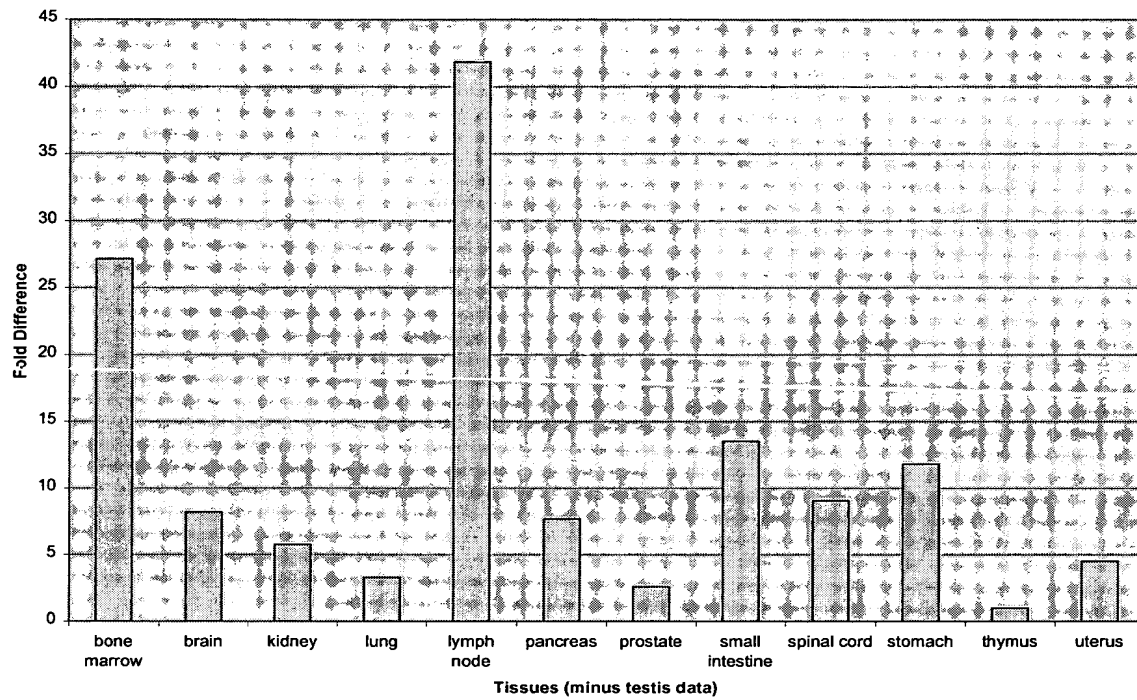


Figure 4.

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
Human membrane channel protein-2	gi Y70452	90.7%	92.5%
Human Maxi-K potassium channel beta subunit	gi 4758625	32.0%	32.0%
Drosophila CG10440 protein	gi 7291303	33.1%	42.6%
Drosophila CG10465 protein	gi 17946205	24.0%	38.8%

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